In the Claims.

Please amend the claims as shown below. This listing of claims will replace all prior versions and listings of the claims in this application.

1-19 (Cancelled).

20. (New) Use in a diagnostic hybridization assay of a probe for lowering the effect of sequence variations in a nucleic acid analyte, which assay comprises the steps of contacting a set of primers and a sample containing the nucleic acid analyte to amplify the analyte and detecting the amplified analyte or its complement by means of the probe, characterized in that the probe comprises:

— one or more nucleotides and/or nucleotide analogues, selected from 2' -O-methyl nucleotides or LNA nucleotides, that have an affinity increasing modification and the diagnostic assay is for assessing the amount of analyte present in the sample, and

— one or more unmodified nucleotides.

21. (New) Use in a diagnostic hybridization assay of a probe for lowering the effect of sequence variations in a nucleic acid analyte, which assay comprises the steps of contacting a set of primers and a sample containing the nucleic acid analyte to amplify the analyte and detecting the amplified analyte or its complement by means of the probe, characterized in that the probe comprises:

— one or more nucleotides and/or nucleotide analogues, selected from 2' -O-methyl nucleotides or LNA nucleotides, that have an affinity increasing modification, i.e. at a constant temperature of hybridization, the melting temperature of the probe with any possible analyte's polymorphism is increased compared to the melting temperature of an unmodified probe with any analyte's polymorphism and the diagnostic assay is for assessing the presence of the analyte in the sample

— one or more unmodified nucleotides.

22. (New) Use as claimed in claim 20, wherein the probe is a molecular beacon.

23. (New) Use as claimed in claim 21, wherein the probe is a molecular beacon.

24. (New) Use in a diagnostic hybridization assay of a molecular beacon probe for lowering the possible opening of the stem of the molecular beacons by way of at least one contaminant present in the amplification enzymes mixture, which assay comprises the steps of contacting a set of primers and a sample containing the nucleic acid analyte to amplify the analyte and detecting the amplified analyte or its complement by means of the probe, characterized in that the probe's stem comprises:

- one or more nucleotides and/or nucleotide analogues that have an affinity increasing modification, especially 2' -O-methyl nucleotides, and
- one or more unmodified nucleotides.

25. (New) Use in a diagnostic hybridization assay of a molecular beacon probe for lowering:

- the effect of sequence variations in a nucleic acid analyte, and/or
- the possible opening of the stem-loop structure of the molecular beacons by way of at least one contaminant present in the amplification enzymes mixture,

which assay comprises the steps of contacting a set of primers and a sample containing the nucleic acid analyte to amplify the analyte and detecting the amplified analyte or its complement by means of the probe, characterized in that the probe's loop comprises:

- one or more nucleotides and/or nucleotide analogues that have an affinity increasing modification, and

— one or more unmodified nucleotides

and/or the probe's stem comprises:

— one or more nucleotides and/or nucleotide analogues that have an affinity increasing modification, especially 2' –O-methyl nucleotides, and

— one or more unmodified nucleotides.

26. (New) Use as claimed in claim 20 wherein the diagnostic assay is a homogenous assay.

27. (New) Use as claimed in claim 21 wherein the diagnostic assay is a homogenous assay.

28. (New) Use as claimed in claim 24 wherein the diagnostic assay is a homogenous assay.

29. (New) Use as claimed in claim 25 wherein the diagnostic assay is a homogenous assay.

30. (New) Use as claimed in claim 20 wherein the diagnostic assay is a heterogeneous assay.

31. (New) Use as claimed in claim 21 wherein the diagnostic assay is a heterogeneous assay.

32. (New) Use as claimed in claim 24 wherein the diagnostic assay is a heterogeneous assay.

33. (New) Use as claimed in claim 25 wherein the diagnostic assay is a heterogeneous assay.

34. (New) Use as claimed in claim 20, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids and peptide nucleic acids.

35. (New) Use as claimed in claim 21, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids and peptide nucleic acids.

36. (New) Use as claimed in claim 24, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids and peptide nucleic acids.

37. (New) Use as claimed in claim 25, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids and peptide nucleic acids.

38. (New) Use as claimed in claim 34, wherein the 2' –O-derivatized nucleotide is a 2' –O-methyl-nucleotide.

39. (New) Molecular beacon probe for use in a diagnostic hybridization assay, said probe comprising one or more nucleotides and/or nucleotide analogues, selected from 2' –O-methyl nucleotides, that have an affinity increasing modification, i.e. at a constant temperature of hybridization, the melting temperature of the probe with any possible analyte's polymorphism is increased compared to the melting temperature of an unmodified probe with the same target.

40. (New) Molecular beacon probe for use in a diagnostic hybridization assay, said probe allowing the lowering of the possible opening of the stem-loop structure of the molecular beacons by way of at least one contaminant present in the amplification enzymes mixture, which assay comprises the steps of contacting a set of primers and a sample containing the nucleic acid analyte to amplify the analyte and detecting the amplified analyte or its complement by means of the probe, characterized in that the probe's stem comprises:

— one or more 2' –methyl nucleotides, and
— one or more unmodified nucleotides.

41. (New) Molecular beacon probe for use in a diagnostic hybridization assay, said probe allowing the lowering of:

— the effect of sequence variations in a nucleic acid analyte, and/or
— the possible opening of the stem-loop structure of the molecular beacons by way of enzymes, characterized in that the probe's loop comprises:
— one or more nucleotides and/or nucleotide analogues that have an affinity increasing modification, and
— one or more unmodified nucleotides

and/or the probe's stem comprises:

— one or more 2' –O-methyl nucleotides, and
— one or more unmodified nucleotides.

42. (New) Probe or molecular beacon probe as claimed in claim 40, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids, and peptide nucleic acids.

43. (New) Probe or molecular beacon probe as claimed in claim 41, wherein the nucleotides or nucleotide analogues having an affinity increasing

modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids, and peptide nucleic acids.

44. (New) Probe or molecular beacon probe as claimed in claim 42, wherein the 2' –O-derivatized nucleotide is a 2' –O-methyl-nucleotide.

45. (New) Molecular beacon probe as claimed in claim 40, wherein each base pair constituting the stem contains no more than one 2' –O-methyl nucleotide.

46. (New) Molecular beacon probe as claimed in claim 41, wherein each base pair constituting the stem contains no more than one 2' –O-methyl nucleotide.

47. (New) Molecular beacon probe as claimed in claim 40, wherein at least one base pair constituting the stem contains no nucleotide or nucleotide analogue having an affinity increasing modification.

48. (New) Molecular beacon probe as claimed in claim 41, wherein at least one base pair constituting the stem contains no nucleotide or nucleotide analogue having an affinity increasing modification.

49. (New) Molecular beacon probe as claimed in claim 40, wherein one base pair constituting the stem contains no nucleotide or nucleotide analogue having an affinity increasing modification.

50. (New) Molecular beacon probe as claimed in claim 41, wherein one base pair constituting the stem contains no nucleotide or nucleotide analogue having an affinity increasing modification.

51. (New) Molecular beacon probe as claimed in claim 40, wherein each strand constituting the stem contains at least one nucleotide or nucleotide analogue having an affinity increasing modification.

52. (New) Molecular beacon probe as claimed in claim 41, wherein each strand constituting the stem contains at least one nucleotide or nucleotide analogue having an affinity increasing modification.

53. (New) Kit for performing a diagnostic amplification assay, comprising the appropriate primers, polymerase(s) and reagents for performing amplification of an analyte to be diagnosed and a probe or a molecular probe as claimed in claim 39 for detecting the amplified analyte.

54. (New) Kit for performing a diagnostic amplification assay, comprising the appropriate primers, polymerase(s) and reagents for performing amplification of an analyte to be diagnosed and a probe or a molecular probe as claimed in claim 40 for detecting the amplified analyte.

55. (New) Kit for performing a diagnostic amplification assay, comprising the appropriate primers, polymerase(s) and reagents for performing amplification of an analyte to be diagnosed and a probe or a molecular probe as claimed in claim 41 for detecting the amplified analyte.